



#5

SEQUENCE LISTING

<110> Prayaga, Sudhirdas
Shimkets, Richard

<120> NOVEL INTERFERON OMEGA AND NUCLEIC ACIDS ENCODING SAME

<130> 15966-615

<140> 09/732,436

<141> 2000-12-07

<150> 60/169,887

<151> 1999-12-09

<150> 60/170,230

<151> 1999-12-10

<160> 22

<170> PatentIn Ver. 2.0

<210> 1

<211> 475

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Curagen clone
AC015663_A

<400> 1

Ala Cys Cys Ala Ala Thr Gly Gly Thr Cys Thr Cys Cys Thr Thr Gly
1 5 10 15

Cys Thr Gly Gly Thr Gly Gly Cys Ala Thr Thr Gly Gly Thr Gly Ala
20 25 30

Thr Gly Ala Thr Cys Thr Cys Cys Thr Gly Cys Cys Ala Cys Ala Thr
35 40 45

Cys Thr Ala Thr Thr Cys Cys Cys Thr Thr Thr Cys Thr Gly Cys
50 55 60

Gly Ala Cys Cys Thr Gly Cys Cys Thr Ala Ala Ala Gly Cys Thr Cys
65 70 75 80

Ala Gly Gly Thr Gly Ala Thr Thr Cys Thr Gly Cys Cys Cys Thr

85

90

95

Cys Cys Ala Thr Ala Ala Gly Ala Thr Gly Cys Ala Cys Cys Ala Gly
100 105 110

Cys Ala Gly Ala Thr Cys Thr Thr Cys Ala Gly Cys Cys Thr Cys Thr
115 120 125

Thr Thr Thr Ala Cys Ala Cys Ala Gly Gly Gly Cys Thr Thr
130 135 140

Gly Thr Cys Thr Gly Ala Thr Gly Cys Thr Thr Gly Gly Ala Ala Thr
145 150 155 160

Ala Gly Gly Cys Cys Thr Thr Cys Cys Thr Gly Gly Ala Cys Ala
165 170 175

Ala Ala Cys Thr Cys Cys Ala Gly Ala Cys Thr Gly Gly Ala Thr Thr
180 185 190

Thr Cys Ala Thr Cys Ala Gly Cys Ala Gly Cys Thr Gly Gly Ala Ala
195 200 205

Gly Ala Cys Cys Thr Gly Gly Ala Gly Ala Cys Cys Thr Gly Cys Thr
210 215 220

Thr Thr Gly Gly Thr Ala Thr Ala Gly Ala Gly Gly Ala Thr Gly Gly
225 230 235 240

Gly Ala Ala Gly Cys Ala Ala Gly Ala Gly Thr Cys Thr Gly Cys Cys
245 250 255

Cys Thr Gly Gly Ala Ala Ala Thr Thr Gly Ala Gly Gly Cys Cys
260 265 270

Cys Thr Ala Cys Ala Cys Thr Gly Gly Cys Cys Ala Thr Ala Ala Ala
275 280 285

Gly Ala Gly Gly Thr Ala Cys Thr Thr Cys Cys Ala Gly Gly Gly Ala
290 295 300

Gly Thr Ala Cys Ala Thr Thr Cys Thr Thr Cys Thr Thr Gly Ala
305 310 315 320

Ala Ala Gly Ala Gly Ala Gly Ala Ala Ala Thr Thr Cys Ala Gly
325 330 335

Gly Ala Ala Cys Thr Gly Thr Ala Cys Cys Thr Gly Gly Ala Gly

340

345

350

Gly Thr Thr Gly Thr Cys Gly Thr Ala Ala Thr Gly Gly Thr Ala Ala
355 360 365

Ala Gly Gly Ala Thr Thr Thr Thr Cys Thr Thr Ala Ala Gly
370 375 380

Cys Ala Cys Ala Ala Ala Ala Cys Thr Thr Cys Ala Ala Gly Ala Ala
385 390 395 400

Ala Ala Ala Gly Ala Gly Ala Ala Cys Ala Gly Ala Ala Gly Ala Ala
405 410 415

Ala Ala Gly Ala Gly Ala Ala Cys Thr Gly Cys Ala Ala Ala Ala
420 425 430

Ala Ala Ala Thr Cys Thr Gly Gly Ala Ala Ala Ala Gly Gly Thr Ala
435 440 445

Ala Thr Cys Thr Ala Thr Thr Thr Ala Gly Cys Ala Gly Ala Ala Gly
450 455 460

Ala Gly Thr Gly Ala Ala Ala Gly Cys Thr Gly
465 470 475

<210> 2

<211> 610

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Curagen clone

<400> 2

Ala Cys Cys Ala Ala Thr Gly Gly Thr Cys Thr Cys Cys Thr Thr Gly
1 5 10 15

Cys Thr Gly Gly Thr Gly Gly Cys Ala Thr Thr Gly Gly Thr Gly Ala
20 25 30

Thr Gly Ala Thr Cys Thr Cys Cys Thr Gly Cys Cys Ala Cys Ala Thr
35 40 45

Cys Thr Ala Thr Thr Cys Cys Cys Thr Thr Thr Cys Thr Gly Cys
50 55 60

Gly Ala Cys Cys Thr Gly Cys Cys Thr Asn Asn Asn Asn Asn Asn
65 70 75 80

Asn
85 90 95

Asn
100 105 110

Asn
115 120 125

Asn
130 135 140

Asn
145 150 155 160

Asn
165 170 175

Asn
180 185 190

Asn
195 200 205

Ala Ala Ala Gly Cys Thr Cys Ala Gly Gly Thr Gly Ala Thr Thr Thr
210 215 220

Cys Thr Gly Cys Cys Cys Thr Cys Cys Ala Thr Ala Ala Gly Ala Thr
225 230 235 240

Gly Cys Ala Cys Cys Ala Gly Cys Ala Gly Ala Thr Cys Thr Thr Cys
245 250 255

Ala Gly Cys Cys Thr Cys Thr Thr Thr Thr Ala Cys Ala Cys Ala
260 265 270

Ala Gly Gly Cys Thr Thr Gly Thr Cys Thr Gly Ala Thr Gly Cys
275 280 285

Thr Thr Gly Gly Ala Ala Thr Ala Gly Gly Cys Cys Thr Thr Cys
290 295 300

Cys Thr Gly Gly Ala Cys Ala Ala Cys Thr Cys Cys Ala Gly Ala
305 310 315 320

Cys Thr Gly Gly Ala Thr Thr Cys Ala Thr Cys Ala Gly Cys Ala
325 330 335

Gly Cys Thr Gly Gly Ala Ala Gly Ala Cys Cys Thr Gly Gly Ala Gly
340 345 350

Ala Cys Cys Thr Gly Cys Thr Thr Gly Gly Thr Ala Thr Ala Gly
355 360 365

Ala Gly Gly Ala Thr Gly Gly Ala Ala Gly Cys Ala Ala Gly Ala
370 375 380

Gly Thr Cys Thr Gly Cys Cys Cys Thr Gly Gly Ala Ala Ala Thr Thr
385 390 395 400

Gly Ala Gly Gly Cys Cys Cys Thr Ala Cys Ala Cys Thr Gly Gly
405 410 415

Cys Cys Ala Thr Ala Ala Ala Gly Ala Gly Gly Thr Ala Cys Thr Thr
420 425 430

Cys Cys Ala Gly Gly Ala Gly Thr Ala Cys Ala Thr Thr Thr Cys
435 440 445

Thr Thr Cys Thr Thr Gly Ala Ala Ala Gly Ala Gly Ala Gly Gly Ala
450 455 460

Ala Ala Thr Thr Cys Ala Gly Gly Ala Ala Cys Thr Gly Thr Ala Cys
465 470 475 480

Cys Thr Gly Gly Ala Gly Gly Thr Thr Gly Thr Cys Gly Thr Ala
485 490 495

Ala Thr Gly Gly Thr Ala Ala Ala Gly Gly Ala Thr Thr Thr Thr
500 505 510

Thr Cys Thr Thr Ala Ala Gly Cys Ala Cys Ala Ala Ala Cys Thr
515 520 525

Thr Cys Ala Ala Gly Ala Ala Ala Ala Gly Ala Gly Ala Ala Cys
530 535 540

Ala Gly Ala Ala Gly Ala Ala Ala Ala Gly Ala Gly Ala Ala Cys Thr
545 550 555 560

Gly Cys Ala Ala Ala Ala Ala Ala Ala Thr Cys Thr Gly Gly Ala
565 570 575

Ala Ala Ala Gly Gly Thr Ala Ala Thr Cys Thr Ala Thr Thr Ala
580 585 590

Gly Cys Ala Gly Ala Ala Gly Ala Gly Thr Gly Ala Ala Ala Gly Cys
595 600 605

Thr Gly
610

<210> 3
<211> 1887
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Curagen clone
AF038458_A

<400> 3
atggccatcc tcccgttgct cctgtgcctg ctggcgctgg cccctgcctc atccccaccc 60
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ctaagcgtgc tgtgcccagg ggcaggcctc ctgttcgtgc caccctcgct ggaccgcccgg 180
gcagccgagc tgcggctggc agacaacttc atgcctccg tgccggcccg cgacacctggcc 240
aacatgacag gcctgctgca tctgagcctg tcgcggaaaca ccattccgcca cgtggctgccc 300
ggcgcccttcg ccgacactgctg ggccctgcgt gccctgcacc tggatggcaa ccggctgacc 360
tcactggcg aggcccagct gcgcggcctg gtcaacttgc gccacccat cctcagcaac 420
aaccagctgg cagcgctggc ggccggccgc ctggatgatt gtgccgagac actggaggac 480
ctcgacacctt cctacaacaa cctcgagcag ctggccctggg aggccctggg ccgcctgggc 540
aacgtcaaca cgttggccct cgaccacaaac ctgtggctt ctgtgcccgc cgccgccttt 600
tcccgcctgc acaagctggc ccggctggac atgacccatcca accgcctgac cacaatccca 660
cccgacccac tcttctcccg cctgcccctg ctgcggcaggc cccggggctc gcccgcctct 720
gccctgggtgc tggcctttgg cgggaaccccc ctgcactgca actgcgagct ggtgtggctg 780
cgtcgcctgg cgccgggagga cgacctcgag gcctgcgcgt ccccacctgc tctgggcggc 840
cgctacttct gggcggtggg cgaggaggag tttgtctgca agccgcccgt ggtgactcac 900
cgctcaccac ctctggctgt gccccgaggt cggccggctg ccctgcgcgt ccgggcagtg 960
ggggacccag agccccgtgt gcgttgggtg tcacccagg gccggctgct aggcaactca 1020
agccgtgccc gcgccttccc caatggacg ctggagctgc tggcaccga gccgggtgat 1080
ggtggcatct tcacccatgc tgcggccaat gcagctggcg aggccacagc tgctgtggag 1140
ctgactgtgg gtccccacc acctccctcag ctgcaccaaca gcaccagctg tgacccccc 1200
cgggacgggg atccctgatgc tctcaccctca ccctccgcgt cctctgcctc tgccaaagggt 1260
gccgacactg ggccccctac cgaccgtggc gtccaggtga ctgagcacgg gcccacagct 1320
gctttgtcc agtggccgga tcagccgcgtt atcccggca tccgcgttgc ccagatccag 1380
tacaacagct cggctgatga catcctcgtc tacaggatga tcccgccgga gagccgcgtc 1440
ttcctgtga cggacactggc gtcaggccgg acctacgatc tggcgtgttgc cggccgtgtat 1500
gaggacagcg ccacggggct cacggccacg cggccgtgtgg gtcgcggcccg cttctccacc 1560
gaacctgcgc tgcggccatg cggggcgccg cacgcctccct tcctggcgg cacgatgatc 1620
atcgcgctgg cggcgctcat cgtagccctg gtactgggttgc tcatcttcgt gctgctaatt 1680

cgctacaagg tgcacggcgg ccagccccc ggcaaggcca agattccgc gcctgttagc 1740
agcgtttgc cccagaccaa cggcgccctg ggccccacgc ccacgcccgc cccgcccccc 1800
ccggagcccg cggcgctcag ggcccacacc gtggtccagc tggactgcga gccctggggg 1860
cccgccacg aacctgtggg accctag 1887

<210> 4
<211> 365
<212> PRT
<213> Equus caballus

<400> 4

Thr	Cys	Cys	Cys	Ala	Gly	Ala	Gly	Gly	Cys	Cys	Cys	Ala	Gly	Gly	Cys
1				5			10					15			

Cys Gly Cys Gly Thr Cys Thr Gly Thr Cys Cys Thr Cys Cys Ala Cys
20 25 30

Gly Ala Gly Ala Thr Gly Cys Thr Cys Cys Ala Gly Cys Ala Gly Ala
35 40 45

Thr Cys Thr Thr Cys Ala Gly Cys Cys Thr Cys Thr Cys Cys Ala
50 55 60

Cys Ala Cys Ala Gly Ala Gly Cys Gly Cys Thr Cys Gly Thr Cys Thr
65 70 75 80

Gly Cys Thr Gly Cys Cys Thr Gly Gly Ala Ala Cys Ala Cys Gly Ala
85 90 95

Cys Cys Cys Thr Cys Cys Thr Gly Gly Ala Cys Gly Ala Ala Cys Thr
100 105 110

Cys Thr Gly Cys Ala Cys Gly Gly Ala Cys Thr Cys Cys Thr Thr
115 120 125

Cys Gly Gly Cys Ala Gly Cys Thr Gly Gly Ala Ala Gly Ala Cys Cys
130 135 140

Thr Gly Gly Ala Cys Ala Cys Cys Thr Gly Thr Thr Thr Gly Gly Ala
145 150 155 160

Gly Cys Ala Gly Gly Ala Gly Ala Thr Gly Gly Gly Ala Gly Ala Gly
165 170 175

Gly Ala Ala Gly Ala Ala Thr Cys Thr Gly Cys Cys Cys Thr Gly Gly
180 185 190

Gly Ala Ala Cys Thr Gly Thr Gly Cys Cys Cys Cys Thr Ala Cys

195

200

205

Ala Cys Thr Gly Gly Cys Cys Gly Thr Gly Ala Ala Gly Ala Gly Gly
210 215 220

Thr Ala Cys Thr Thr Cys Cys Gly Gly Gly Gly Ala Thr Cys Cys
225 230 235 240

Ala Thr Cys Thr Cys Thr Ala Cys Cys Thr Gly Ala Ala Ala Gly Ala
245 250 255

Gly Ala Ala Gly Ala Ala Ala Thr Ala Cys Ala Gly Thr Gly Ala Cys
260 265 270

Thr Gly Thr Gly Cys Cys Thr Gly Gly Gly Ala Gly Ala Thr Thr Gly
275 280 285

Thr Cys Cys Gly Ala Ala Thr Gly Gly Ala Ala Ala Thr Cys Ala Thr
290 295 300

Gly Ala Gly Ala Thr Cys Cys Thr Thr Cys Thr Cys Thr Thr Cys Ala
305 310 315 320

Thr Cys Ala Gly Cys Ala Ala Ala Cys Cys Thr Gly Cys Ala Ala Gly
325 330 335

Gly Ala Ala Gly Gly Thr Thr Ala Ala Gly Ala Ala Thr Gly Ala Ala
340 345 350

Gly Gly Ala Thr Gly Gly Ala Gly Ala Cys Cys Thr Gly
355 360 365

<210> 5

<211> 132

<212> PRT

<213> Homo sapiens

<400> 5

Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr
1 5 10 15

Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu
20 25 30

Leu Ser Arg Asn Thr Leu Val Phe Pro Gln Glu Met Val Lys Gly Ser
35 40 45

Gln Leu Gln Lys Ala His Val Met Ser Val Leu His Glu Met Leu Gln
50 55 60

Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser Ser Ala Ala Thr Cys
65 70 75 80

Leu Leu Gln Val Val Gly Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser
85 90 95

Pro Ala Leu Thr Leu Arg Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu
100 105 110

Lys Glu Lys Lys Tyr Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp
115 120 125

Leu Gly Ser Ser
130

<210> 6

<211> 132

<212> PRT

<213> Equus caballus

<400> 6

Met Ala Phe Ser Val Ser Ser Leu Met Ala Leu Val Val Ile Ser Ser
1 5 10 15

Ser Pro Val Ser Ser Met Ser Cys Asp Leu Pro Ala Ser Leu Asp Leu
20 25 30

Arg Lys Gln Glu Thr Leu Arg Phe Pro Gln Glu Gln Leu Asp Gly Arg
35 40 45

Gln Phe Pro Glu Ala Gln Ala Thr Ser Val Leu Gln Glu Met Leu Gln
50 55 60

Gln Ile Val Ser Leu Phe His Thr Glu Arg Ser Ser Ala Ala Thr Cys
65 70 75 80

Leu Asp Glu Gln Thr Gly Glu Glu Ser Ala Leu Gly Thr Val Gly
85 90 95

Pro Thr Leu Ala Val Lys Arg Tyr Phe Arg Arg Ile Arg Leu Tyr Leu
100 105 110

Thr Glu Lys Lys Tyr Leu Gln Gly Arg Leu Gly Met Lys Asp Gly Asp
115 120 125

Leu Gly Ser Pro
130

<210> 7
<211> 475
<212> PRT
<213> Homo sapiens

<400> 7
Ala Cys Cys Ala Ala Thr Gly Gly Thr Cys Thr Cys Cys Thr Thr Gly
1 5 10 15

Cys Thr Gly Gly Thr Gly Gly Cys Ala Thr Thr Gly Gly Thr Gly Ala
20 25 30

Thr Gly Ala Thr Cys Thr Cys Cys Thr Gly Cys Cys Ala Cys Ala Thr
35 40 45

Cys Thr Ala Thr Thr Cys Cys Cys Thr Thr Thr Cys Thr Gly Cys
50 55 60

Gly Ala Cys Cys Thr Gly Cys Cys Thr Ala Ala Ala Gly Cys Thr Cys
65 70 75 80

Ala Gly Gly Thr Gly Ala Thr Thr Cys Thr Gly Cys Cys Cys Thr
85 90 95

Cys Cys Ala Thr Ala Ala Gly Ala Thr Gly Cys Ala Cys Cys Ala Gly
100 105 110

Cys Ala Gly Ala Thr Cys Thr Thr Cys Ala Gly Cys Cys Thr Cys Thr
115 120 125

Thr Thr Thr Ala Cys Ala Cys Ala Gly Gly Cys Thr Thr
130 135 140

Gly Thr Cys Thr Gly Ala Thr Gly Cys Thr Thr Gly Gly Ala Ala Thr
145 150 155 160

Ala Gly Gly Cys Cys Thr Thr Cys Cys Thr Gly Gly Ala Cys Ala
165 170 175

Ala Ala Cys Thr Cys Cys Ala Gly Ala Cys Thr Gly Gly Ala Thr Thr
180 185 190

Thr Cys Ala Thr Cys Ala Gly Cys Ala Gly Cys Thr Gly Gly Ala Ala

195

200

205

Gly Ala Cys Cys Thr Gly Gly Ala Gly Ala Cys Cys Thr Gly Cys Thr
210 215 220

Thr Thr Gly Gly Thr Ala Thr Ala Gly Gly Ala Thr Gly Gly
225 230 235 240

Gly Ala Ala Gly Cys Ala Ala Gly Ala Gly Thr Cys Thr Gly Cys Cys
245 250 255

Cys Thr Gly Gly Ala Ala Ala Thr Thr Gly Ala Gly Gly Cys Cys
260 265 270

Cys Thr Ala Cys Ala Cys Thr Gly Gly Cys Cys Ala Thr Ala Ala Ala
275 280 285

Gly Ala Gly Gly Thr Ala Cys Thr Thr Cys Cys Ala Gly Gly Ala
290 295 300

Gly Thr Ala Cys Ala Thr Thr Cys Thr Thr Cys Thr Thr Gly Ala
305 310 315 320

Ala Ala Gly Ala Gly Ala Gly Ala Ala Ala Thr Thr Cys Ala Gly
325 330 335

Gly Ala Ala Cys Thr Gly Thr Ala Cys Cys Thr Gly Gly Ala Gly
340 345 350

Gly Thr Thr Gly Thr Cys Gly Thr Ala Ala Thr Gly Gly Thr Ala Ala
355 360 365

Ala Gly Gly Ala Thr Thr Thr Cys Thr Thr Ala Ala Gly
370 375 380

Cys Ala Cys Ala Ala Ala Ala Cys Thr Thr Cys Ala Ala Gly Ala Ala
385 390 395 400

Ala Ala Ala Gly Ala Gly Ala Ala Cys Ala Gly Ala Ala Gly Ala Ala
405 410 415

Ala Ala Gly Ala Gly Ala Ala Cys Thr Gly Cys Ala Ala Ala Ala Ala
420 425 430

Ala Ala Ala Thr Cys Thr Gly Gly Ala Ala Ala Ala Gly Gly Thr Ala
435 440 445

Ala Thr Cys Thr Ala Thr Thr Ala Gly Cys Ala Gly Ala Ala Gly

450

455

460

Ala Gly Thr Gly Ala Ala Ala Gly Cys Thr Gly
465 470 475

<210> 8
<211> 70
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism: Interferon Alpha
Precursor

<400> 8
shkaasvvhv tnkhctasss aawnttctgd rtracvvgat ndhdsrnyrs ykkyscawvr 60
amrsyyssta 70

<210> 9
<211> 112
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: Interferon
Delta-1 Precursor

<400> 9
Leu Gln Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln
1 5 10 15

Ser Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr
20 25 30

Thr Leu Leu Glu Pro Cys Arg Thr Gly Leu His Gln Gln Leu Asp Asn
35 40 45

Leu Asp Ala Cys Leu Gly Gln Val Met Gly Glu Glu Asp Ser Ala Leu
50 55 60

Gly Arg Thr Gly Pro Thr Leu Ala Leu Lys Arg Tyr Phe Gln Gly Ile
65 70 75 80

His Val Tyr Leu Lys Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Thr
85 90 95

Val Arg Leu Glu Ile Met Arg Ser Phe Ser Ser Leu Ile Ser Leu Gln

100

105

110

<210> 10
<211> 112
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: Interferon
Omega-2 Precursor (Interferon Alpha-II-2)

<400> 10
Phe Pro Glu Ala Gln Ala Ala Ser Val Leu His Glu Met Leu Gln Gln
1 5 10 15

Ile Phe Ser Leu Phe His Thr Glu Arg Ser Ser Ala Ala Trp Asn Thr
20 25 30

Thr Leu Leu Asp Glu Leu Cys Thr Gly Leu Leu Arg Gln Leu Glu Asp
35 40 45

Leu Asp Thr Cys Leu Glu Gln Glu Met Gly Glu Glu Ser Ala Leu
50 55 60

Gly Thr Val Arg Pro Thr Leu Ala Val Lys Arg Tyr Phe Arg Gly Ile
65 70 75 80

His Leu Tyr Leu Lys Glu Lys Tyr Ser Asp Cys Ala Trp Glu Ile
85 90 95

Val Arg Met Glu Ile Met Arg Ser Phe Ser Ser Ser Ala Asn Leu Gln
100 105 110

<210> 11
<211> 112
<212> PRT
<213> Unknown

<400> 11
Leu Gln Lys Ala His Val Met Ser Val Leu His Glu Met Leu Gln Gln

1 5 10 15

Ile Phe Ser Leu Phe His Thr Glu Arg Ser Ser Ala Ala Trp Asn Met
20 25 30

Thr Leu Leu Asp Gln Leu His Thr Gly Leu His Gln Gln Leu Gln His
35 40 45

Leu Glu Thr Cys Leu Leu Gln Val Val Gly Glu Gly Glu Ser Ala Gly
50 55 60

Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg Arg Tyr Phe Gln Gly Ile
65 70 75 80

Arg Val Tyr Leu Lys Glu Lys Tyr Ser Asp Cys Ala Trp Glu Val
85 90 95

Val Arg Met Glu Ile Met Lys Ser Leu Phe Leu Ser Thr Asn Met Gln
100 105 110

<210> 12

<211> 65

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: Interferon

<400> 12

Ala Gln Ser Val Leu His Met Gln Gln Ile Phe Leu Phe Thr Glu Ser
1 5 10 15

Ser Ala Ala Trp Asn Thr Leu Leu Thr Gly Leu Gln Leu Leu Cys Gln
20 25 30

Gly Glu Glu Ser Ala Leu Pro Leu Arg Tyr Phe Gln Gly Tyr Leu Lys
35 40 45

Glu Lys Lys Tyr Ser Cys Ala Trp Glu Val Arg Glu Ile Met Ser Leu
50 55 60

Gln

65

<210> 13
<211> 110
<212> PRT
<213> Homo sapiens

<400> 13

Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys
1 5 10 15

Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala
20 25 30

Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val
35 40 45

Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr
50 55 60

Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu
65 70 75 80

Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr
85 90 95

Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val
100 105 110

<210> 14
<211> 109
<212> PRT
<213> Homo sapiens

<400> 14

Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln Lys Ala
1 5 10 15

Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe Asn Leu
20 25 30

Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu Leu Asp
35 40 45

Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys
50 55 60

Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Asn Glu Asp

65	70	75	80
Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu Tyr Leu			
85		90	95
Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val			
100	105		
<210> 15			
<211> 110			
<212> PRT			
<213> Unknown			
<220>			
<223> Description of Unknown Organism: Interferon			
Alpha-1 Precursor			
<400> 15			
Asp Phe Gly Phe Pro Gln Glu Lys Val Asp Ala Gln Gln Ile Lys Lys			
1	5	10	15
Ala Gln Ala Ile Pro Val Leu Ser Glu Leu Thr Gln Gln Ile Leu Asn			
20	25	30	
Ile Phe Thr Ser Lys Asp Ser Ser Ala Ala Trp Asn Ala Thr Leu Leu			
35	40	45	
Asp Ser Phe Cys Asn Asp Leu His Gln Gln Leu Asn Asp Leu Gln Gly			
50	55	60	
Cys Leu Met Gln Gln Val Gly Val Gln Glu Phe Pro Leu Thr Gln Glu			
65	70	75	80
Asp Ala Leu Leu Ala Val Arg Lys Tyr Phe His Arg Ile Thr Val Tyr			
85	90	95	
Leu Arg Glu Lys Lys His Ser Pro Cys Ala Trp Glu Val Val			
100	105	110	
<210> 16			
<211> 110			
<212> PRT			
<213> Rabbitt Interferon-omega20			
<400> 16			
Asp Phe Gln Phe Pro Arg Glu Val Val Asn Gly Ser Gln Phe Gln Lys			

1 5 10 15

Asn Gln Thr Val Ser Val Leu His Glu Met Leu Gln Gln Ile Phe Asn
20 25 30

Leu Leu His Thr Ala Arg Ser Ser Ala Ala Trp Asn Asn Thr Leu Leu
35 40 45

Glu Glu Leu His Thr Ala Leu His Gln Gln Leu Gln Gly Leu Glu Thr
50 55 60

Cys Leu Val Gln Ala Met Gly Glu Glu Asp Ser Val Leu Thr Ala Asp
65 70 75 80

Ser Pro Met Leu Met Leu Lys Arg Tyr Phe Gln Arg Ile Arg Leu Tyr
85 90 95

Leu Asp Glu Lys Lys His Ser Gly Cys Ala Trp Glu Leu Val
100 105 110

<210> 17

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Concensus of
SEQ ID NO:1 and SEQ ID NOS:16-19

<400> 17

Phe Pro Glu Gln Lys Leu Glu Met Gln Gln Ile Phe Phe Ser Ser Ala
1 5 10 15

Trp Asn Thr Leu Gln Gln Leu Leu Cys Gly Leu Leu Tyr Phe Arg Ile
20 25 30

Tyr Leu Glu Lys Lys Ser Cys Ala Trp Glu Val
35 40

<210> 18

<211> 184

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: Interferon

Alpha-1 Precursor

<400> 18
Val Ser Leu Leu Met Ala Leu Val Val Leu Ser Cys His Ser Ile Cys
1 5 10 15

Ser Leu Gly Cys Asp Leu Pro His Thr His Ser Leu Gly Asn Thr Arg
20 25 30

Val Leu Met Leu Leu Gly Gln Met Arg Arg Ile Ser Pro Phe Ser Cys
35 40 45

Leu Lys Asp Arg Asn Asp Phe Gly Phe Pro Gln Glu Val Phe Asp Gly
50 55 60

Asn Gln Phe Arg Lys Pro Gln Ala Ile Ser Ala Val His Glu Thr Ile
65 70 75 , 80

Gln Gln Ile Phe His Leu Phe Ser Thr Asp Gly Ser Ser Ala Ala Trp
85 90 95

Asp Glu Ser Leu Leu Asp Lys Leu Tyr Thr Gly Leu Tyr Gln Gln Leu
100 105 110

Thr Glu Leu Glu Ala Cys Leu Ser Gln Glu Val Gly Val Glu Glu Thr
115 120 125

Pro Leu Met Asn Glu Asp Ser Leu Leu Ala Val Arg Arg Tyr Phe Gln
130 135 140

Arg Ile Ala Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp
145 150 155 160

Glu Ile Val Arg Ala Glu Ile Met Arg Ser Phe Ser Ser Ser Thr Asn
165 170 175

Leu Pro Ser Glu Gln Ile Asp Asn
180

<210> 19
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus of
SEQ ID NO:4 and SEQ ID NOS:11, 13, 14, 21 and 22

<400> 19

Ser Leu Leu Ala Leu Val Ser Leu Gly Cys Asp Leu Pro His Leu Leu
1 5 10 15

Leu Gln Met Arg Cys Lys Asp Arg Asp Phe Phe Pro Gln Gly Gln Lys
20 25 30

Ala Gln Ser His Gln Gln Ile Phe Leu Phe Thr Ser Ser Ala Ala Trp
35 40 45

Asn Leu Leu Asp Leu Thr Gly Leu Gln Leu Leu Glu Cys Gln Glu Gly
50 55 60

Glu Leu Leu Arg Tyr Phe Gln Tyr Leu Glu Lys Lys Tyr Ser Cys Ala
65 70 75 80

Trp Glu Val Arg Glu Ile Met Ser Ser Thr Leu Gln
85 90

<210> 20

<211> 1752

<212> PRT

<213> Homo sapiens

<400> 20

Cys Gly Cys Cys Thr Gly Cys Cys Cys Cys Ala Ala Gly Thr Ala Cys
1 5 10 15

Thr Gly Thr Gly Thr Cys Thr Gly Cys Cys Ala Gly Ala Ala Thr Cys
20 25 30

Thr Gly Thr Cys Thr Gly Ala Gly Thr Cys Ala Cys Thr Gly Gly Gly
35 40 45

Gly Ala Cys Cys Cys Thr Gly Thr Gly Cys Cys Cys Cys Thr Cys Cys
50 55 60

Ala Ala Gly Gly Gly Cys Thr Gly Cys Thr Cys Thr Thr Thr Gly
65 70 75 80

Thr Ala Cys Cys Cys Cys Cys Thr Gly Ala Thr Ala Thr Thr Gly Ala
85 90 95

Cys Cys Gly Gly Cys Gly Ala Cys Ala Gly Thr Gly Gly Ala Gly
100 105 110

Cys Thr Gly Cys Gly Cys Cys Thr Gly Gly Gly Cys Gly Cys Ala
115 120 125

Ala Cys Thr Thr Cys Ala Thr Cys Ala Thr Cys Cys Ala Cys Ala Thr
130 135 140

Cys Ala Gly Cys Cys Gly Cys Cys Ala Gly Gly Ala Cys Thr Thr Thr
145 150 155 160

Gly Cys Cys Ala Ala Cys Ala Thr Gly Ala Cys Gly Gly Gly Cys
165 170 175

Thr Gly Gly Thr Gly Gly Ala Cys Cys Thr Gly Ala Cys Cys Cys Thr
180 185 190

Gly Thr Cys Cys Ala Gly Gly Ala Ala Cys Ala Cys Cys Ala Thr Cys
195 200 205

Ala Gly Cys Cys Ala Cys Ala Thr Cys Cys Ala Gly Cys Cys Cys Thr
210 215 220

Thr Thr Thr Cys Cys Thr Thr Thr Cys Thr Gly Gly Ala Cys Cys Thr
225 230 235 240

Cys Gly Ala Gly Ala Gly Cys Cys Thr Cys Cys Gly Cys Thr Cys Cys
245 250 255

Cys Thr Gly Cys Ala Thr Cys Thr Gly Ala Cys Ala Gly Cys Ala
260 265 270

Ala Thr Cys Gly Gly Cys Thr Gly Cys Cys Ala Ala Gly Cys Cys Thr
275 280 285

Thr Gly Gly Gly Ala Gly Gly Ala Cys Ala Cys Cys Cys Thr Cys
290 295 300

Cys Gly Gly Gly Cys Cys Thr Gly Gly Thr Cys Ala Ala Cys Cys
305 310 315 320

Thr Gly Cys Ala Gly Cys Ala Cys Cys Thr Thr Ala Thr Cys Gly Thr
325 330 335

Gly Ala Ala Cys Ala Ala Cys Ala Ala Cys Cys Ala Gly Cys Thr Gly
340 345 350

Gly Gly Cys Gly Gly Cys Ala Thr Cys Gly Cys Ala Gly Ala Thr Gly
355 360 365

Ala Gly Gly Cys Thr Thr Thr Gly Ala Gly Gly Ala Cys Thr Thr
370 375 380

Cys Cys Thr Gly Cys Thr Gly Ala Cys Ala Thr Thr Gly Gly Ala Gly
385 390 395 400

Gly Ala Thr Cys Thr Gly Gly Ala Cys Cys Thr Cys Thr Cys Cys Thr
405 410 415

Ala Cys Ala Ala Cys Ala Ala Cys Cys Thr Cys Cys Ala Thr Gly Gly
420 425 430

Cys Cys Thr Gly Cys Cys Gly Thr Gly Gly Ala Cys Thr Cys Cys
435 440 445

Gly Thr Gly Cys Gly Ala Cys Gly Cys Ala Thr Gly Gly Thr Cys Ala
450 455 460

Ala Cys Cys Thr Cys Cys Ala Cys Cys Ala Gly Cys Thr Gly Ala Gly
465 470 475 480

Cys Cys Thr Gly Gly Ala Cys Cys Ala Cys Ala Ala Cys Cys Thr Gly
485 490 495

Cys Thr Gly Gly Ala Thr Cys Ala Cys Ala Thr Cys Gly Cys Cys Gly
500 505 510

Ala Gly Gly Cys Ala Cys Cys Thr Thr Thr Gly Cys Ala Gly Ala
515 520 525

Cys Cys Thr Gly Cys Ala Gly Ala Ala Ala Cys Thr Gly Gly Cys Cys
530 535 540

Cys Gly Cys Cys Thr Gly Gly Ala Thr Cys Thr Cys Ala Cys Cys Thr
545 550 555 560

Cys Cys Ala Ala Thr Cys Gly Gly Cys Thr Gly Cys Ala Gly Ala Ala
565 570 575

Gly Cys Thr Gly Cys Cys Cys Cys Cys Thr Gly Ala Thr Cys Cys Cys
580 585 590

Ala Thr Cys Thr Thr Thr Gly Cys Cys Gly Cys Thr Cys Cys Cys
595 600 605

Ala Gly Gly Cys Thr Thr Cys Gly Gly Cys Thr Thr Thr Gly Ala Cys
610 615 620

Ala Gly Cys Cys Ala Cys Ala Cys Cys Cys Thr Thr Thr Gly Cys Cys
625 630 635 640

Cys Cys Ala Cys Cys Cys Thr Thr Gly Thr Cys Cys Thr Thr Ala
645 650 655

Gly Thr Thr Thr Gly Gly Gly Gly Thr Ala Ala Cys Cys Cys
660 665 670

Ala Cys Thr Thr Cys Ala Cys Thr Gly Cys Ala Ala Thr Thr Gly Thr
675 680 685

Gly Ala Gly Cys Thr Thr Cys Thr Gly Gly Cys Thr Gly Cys
690 695 700

Gly Gly Ala Gly Gly Cys Thr Cys Gly Ala Gly Cys Gly Gly Ala
705 710 715 720

Cys Gly Ala Thr Gly Ala Cys Cys Thr Gly Gly Ala Ala Ala Cys Cys
725 730 735

Thr Gly Thr Gly Gly Cys Thr Cys Cys Cys Ala Gly Gly Gly
740 745 750

Gly Cys Cys Thr Cys Ala Ala Gly Gly Gly Thr Cys Gly Cys Thr Ala
755 760 765

Cys Thr Thr Cys Thr Gly Gly Cys Ala Thr Gly Thr Gly Cys Gly Thr
770 775 780

Gly Ala Gly Gly Ala Gly Gly Ala Gly Thr Thr Gly Thr Gly Thr
785 790 795 800

Gly Cys Gly Ala Gly Cys Cys Gly Cys Cys Thr Cys Thr Cys Ala Thr
805 810 815

Cys Ala Cys Cys Cys Ala Gly Cys Ala Cys Ala Cys Ala Cys
820 825 830

Ala Ala Gly Thr Thr Gly Cys Thr Gly Gly Thr Thr Cys Thr Gly Gly
835 840 845

Ala Gly Gly Cys Cys Ala Gly Gly Cys Gly Gly Cys Cys Ala Cys
850 855 860

Ala Cys Thr Cys Ala Ala Gly Thr Gly Cys Ala Ala Ala Gly Cys Cys
865 870 875 880

Ala Thr Thr Gly Gly Gly Ala Cys Cys Cys Cys Ala Gly Cys Cys
885 890 895

Cys Cys Cys Thr Thr Ala Thr Cys Cys Ala Cys Thr Gly Gly Gly Thr
900 905 910

Ala Gly Cys Cys Cys Cys Cys Gly Ala Thr Gly Ala Cys Cys Gly Cys
915 920 925

Cys Thr Gly Gly Thr Ala Gly Gly Ala Ala Cys Thr Cys Cys Thr
930 935 940

Cys Ala Ala Gly Gly Ala Cys Cys Gly Cys Thr Gly Thr Cys Thr Ala
945 950 955 960

Thr Gly Ala Cys Ala Ala Thr Gly Gly Cys Ala Cys Cys Cys Thr Gly
965 970 975

Gly Ala Cys Ala Thr Cys Thr Cys Ala Thr Cys Ala Cys Cys Ala
980 985 990

Cys Ala Thr Cys Thr Cys Ala Gly Gly Ala Cys Ala Gly Thr Gly Gly
995 1000 1005

Thr Gly Cys Cys Thr Thr Cys Ala Cys Cys Thr Gly Cys Ala Thr Thr
1010 1015 1020

Gly Cys Thr Gly Cys Cys Ala Ala Thr Gly Cys Thr Gly Cys Cys Gly
1025 1030 1035 1040

Gly Ala Gly Ala Gly Gly Cys Cys Ala Cys Gly Gly Cys Cys Ala Thr
1045 1050 1055

Gly Gly Thr Gly Ala Gly Gly Thr Cys Thr Cys Cys Ala Thr Cys
1060 1065 1070

Gly Thr Cys Cys Ala Gly Cys Thr Gly Cys Cys Ala Cys Cys
1075 1080 1085

Thr Cys Ala Gly Cys Ala Ala Cys Ala Gly Cys Ala Cys Cys Ala Gly
1090 1095 1100

Cys Cys Gly Cys Ala Cys Thr Gly Cys Ala Cys Cys Cys Cys Cys
1105 1110 1115 1120

Ala Ala Gly Thr Cys Cys Cys Gly Cys Cys Thr Cys Thr Cys Ala Gly
1125 1130 1135

Ala Cys Ala Thr Cys Ala Cys Thr Gly Gly Cys Thr Cys Cys Ala Gly
1140 1145 1150

Cys Ala Ala Gly Ala Cys Cys Ala Gly Cys Cys Gly Gly Gly Ala
1155 1160 1165

Gly Gly Thr Gly Gly Ala Gly Gly Cys Ala Gly Thr Gly Gly Gly
1170 1175 1180

Gly Cys Gly Gly Ala Gly Ala Gly Cys Cys Thr Cys Cys Cys Ala Ala
1185 1190 1195 1200

Ala Ala Gly Cys Cys Cys Cys Cys Gly Gly Ala Ala Cys Gly Gly
1205 1210 1215

Gly Cys Thr Gly Thr Gly Cys Thr Thr Gly Thr Gly Thr Cys Thr Gly
1220 1225 1230

Ala Ala Gly Thr Gly Ala Cys Cys Ala Cys Cys Ala Cys Thr Cys
1235 1240 1245

Gly Gly Cys Cys Cys Thr Gly Gly Thr Cys Ala Ala Gly Thr Gly Gly
1250 1255 1260

Thr Cys Thr Gly Thr Cys Ala Gly Cys Ala Ala Gly Thr Cys Ala Gly
1265 1270 1275 1280

Cys Ala Cys Cys Cys Cys Gly Gly Thr Gly Ala Ala Gly Ala Thr
1285 1290 1295

Gly Thr Ala Cys Cys Ala Gly Cys Thr Gly Cys Ala Gly Thr Ala Cys
1300 1305 1310

Ala Ala Cys Thr Gly Cys Thr Cys Thr Gly Ala Cys Gly Ala Thr Gly
1315 1320 1325

Ala Gly Gly Thr Ala Cys Thr Gly Ala Thr Thr Ala Cys Ala Gly
1330 1335 1340

Gly Ala Thr Gly Ala Thr Cys Cys Ala Gly Cys Cys Thr Cys Cys
1345 1350 1355 1360

Ala Ala Cys Ala Ala Gly Gly Cys Cys Thr Thr Cys Gly Thr Gly Gly
1365 1370 1375

Thr Cys Ala Ala Cys Ala Ala Cys Cys Thr Gly Gly Thr Gly Thr Cys
1380 1385 1390

Ala Gly Gly Ala Cys Thr Gly Gly Cys Thr Ala Cys Gly Ala Cys
1395 1400 1405

Thr Thr Gly Thr Gly Thr Gly Cys Thr Gly Gly Cys Cys Ala
1410 1415 1420

Thr Gly Thr Gly Gly Ala Thr Gly Ala Cys Ala Cys Ala Gly Cys
1425 1430 1435 1440

Cys Ala Cys Gly Ala Cys Ala Cys Thr Cys Ala Cys Gly Gly Cys Cys
1445 1450 1455

Ala Cys Cys Ala Ala Cys Ala Thr Cys Gly Thr Gly Gly Cys Thr
1460 1465 1470

Gly Cys Gly Cys Cys Cys Ala Gly Thr Thr Cys Thr Thr Cys Ala Cys
1475 1480 1485

Cys Ala Ala Gly Gly Cys Thr Gly Ala Cys Thr Ala Cys Cys Cys Gly
1490 1495 1500

Cys Ala Gly Thr Gly Cys Cys Ala Gly Thr Cys Cys Ala Thr Gly Cys
1505 1510 1515 1520

Ala Cys Ala Gly Cys Cys Ala Gly Ala Thr Thr Cys Thr Gly Gly Gly
1525 1530 1535

Cys Gly Gly Cys Ala Cys Cys Ala Thr Gly Ala Thr Cys Cys Thr Gly
1540 1545 1550

Gly Thr Cys Ala Thr Cys Gly Gly Gly Gly Cys Ala Thr Cys Ala
1555 1560 1565

Thr Cys Gly Thr Gly Gly Cys Cys Ala Cys Gly Cys Thr Gly Cys Thr
1570 1575 1580

Gly Gly Thr Cys Thr Thr Cys Ala Thr Cys Gly Thr Cys Ala Thr Cys
1585 1590 1595 1600

Cys Thr Cys Ala Thr Gly Gly Thr Gly Cys Gly Cys Thr Ala Cys Ala
1605 1610 1615

Ala Gly Gly Thr Cys Thr Gly Cys Ala Ala Cys Cys Ala Cys Gly Ala
1620 1625 1630

Gly Gly Cys Cys Cys Cys Cys Ala Gly Cys Ala Ala Gly Ala Thr Gly
1635 1640 1645

Gly Cys Ala Gly Cys Gly Gly Cys Cys Gly Thr Gly Ala Gly Cys Ala
1650 1655 1660

Ala Thr Gly Thr Gly Thr Ala Cys Thr Cys Gly Cys Ala Gly Ala Cys
1665 1670 1675 1680

Cys Ala Ala Cys Gly Gly Cys Gly Cys Cys Ala Gly Cys Cys Ala
1685 1690 1695

Cys Cys Gly Cys Cys Thr Cys Cys Ala Ala Gly Cys Ala Gly Cys Gly
1700 1705 1710

Cys Ala Cys Cys Ala Gly Cys Cys Gly Gly Gly Cys Cys Cys Cys
1715 1720 1725

Gly Cys Cys Gly Cys Ala Gly Gly Cys Cys Cys Gly Cys Cys Gly
1730 1735 1740

Ala Ala Gly Gly Thr Gly Gly Thr
1745 1750

<210> 21

<211> 581

<212> PRT

<213> Homo sapiens

<400> 21

Ala Val Val Asp Ala Cys Pro Lys Tyr Cys Val Cys Gln Asn Leu Ser
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Glu Ser Leu Gly Thr Leu Cys Pro Ser Lys Gly Leu Leu Phe Val Pro
20 25 30

Pro Asp Ile Asp Arg Arg Thr Val Glu Leu Arg Leu Gly Gly Asn Phe
35 40 45

Ile Ile His Ile Ser Arg Gln Asp Phe Ala Asn Met Thr Gly Leu Val
50 55 60

Asp Leu Thr Leu Ser Arg Asn Thr Ile Ser His Ile Gln Pro Phe Ser
65 70 75 80

Phe Leu Asp Leu Glu Ser Leu Arg Ser Leu His Leu Asp Ser Asn Arg
85 90 95

Leu Pro Ser Leu Gly Glu Asp Thr Leu Arg Gly Leu Val Asn Leu Gln
100 105 110

His	Leu	Ile	Val	Asn	Asn	Asn	Gln	Leu	Gly	Gly	Ile	Ala	Asp	Glu	Ala
115							120					125			
Phe	Glu	Asp	Phe	Leu	Leu	Thr	Leu	Glu	Asp	Leu	Asp	Leu	Ser	Tyr	Asn
130							135					140			
Asn	Leu	His	Gly	Leu	Pro	Trp	Asp	Ser	Val	Arg	Arg	Met	Val	Asn	Leu
145							150			155			160		
His	Gln	Leu	Ser	Leu	Asp	His	Asn	Leu	Leu	Asp	His	Ile	Ala	Glu	Gly
	165							170					175		
Thr	Phe	Ala	Asp	Leu	Gln	Lys	Leu	Ala	Arg	Leu	Asp	Leu	Thr	Ser	Asn
	180						185					190			
Arg	Leu	Gln	Lys	Leu	Pro	Pro	Asp	Pro	Ile	Phe	Ala	Arg	Ser	Gln	Ala
	195						200					205			
Ser	Ala	Leu	Thr	Ala	Thr	Pro	Phe	Ala	Pro	Pro	Leu	Ser	Phe	Ser	Phe
	210					215					220				
Gly	Gly	Asn	Pro	Leu	His	Cys	Asn	Cys	Glu	Leu	Leu	Trp	Leu	Arg	Arg
	225					230				235			240		
Leu	Glu	Arg	Asp	Asp	Asp	Leu	Glu	Thr	Cys	Gly	Ser	Pro	Gly	Gly	Leu
	245						250					255			
Lys	Gly	Arg	Tyr	Phe	Trp	His	Val	Arg	Glu	Glu	Glu	Phe	Val	Cys	Glu
	260						265					270			
Pro	Pro	Leu	Ile	Thr	Gln	His	Thr	His	Lys	Leu	Leu	Val	Leu	Glu	Gly
	275						280					285			
Gln	Ala	Ala	Thr	Leu	Lys	Cys	Lys	Ala	Ile	Gly	Asp	Pro	Ser	Pro	Leu
	290						295					300			
Ile	His	Trp	Val	Ala	Pro	Asp	Asp	Arg	Leu	Val	Gly	Asn	Ser	Ser	Arg
	305						310				315		320		
Thr	Ala	Val	Tyr	Asp	Asn	Gly	Thr	Leu	Asp	Ile	Phe	Ile	Thr	Thr	Ser
	325							330				335			
Gln	Asp	Ser	Gly	Ala	Phe	Thr	Cys	Ile	Ala	Ala	Asn	Ala	Ala	Gly	Glu
	340						345					350			
Ala	Thr	Ala	Met	Val	Glu	Val	Ser	Ile	Val	Gln	Leu	Pro	His	Leu	Ser
	355						360					365			

Asn Ser Thr Ser Arg Thr Ala Pro Pro Lys Ser Arg Leu Ser Asp Ile
370 375 380

Thr Gly Ser Ser Lys Thr Ser Arg Gly Gly Gly Ser Gly Gly Gly
385 390 395 400

Glu Pro Pro Lys Ser Pro Pro Glu Arg Ala Val Leu Val Ser Glu Val
405 410 415

Thr Thr Thr Ser Ala Leu Val Lys Trp Ser Val Ser Lys Ser Ala Pro
420 425 430

Arg Val Lys Met Tyr Gln Leu Gln Tyr Asn Cys Ser Asp Asp Glu Val
435 440 445

Leu Ile Tyr Arg Met Ile Pro Ala Ser Asn Lys Ala Phe Val Val Asn
450 455 460

Asn Leu Val Ser Gly Thr Gly Tyr Asp Leu Cys Val Leu Ala Met Trp
465 470 475 480

Asp Asp Thr Ala Thr Thr Leu Thr Ala Thr Asn Ile Val Gly Cys Ala
485 490 495

Gln Phe Phe Thr Lys Ala Asp Tyr Pro Gln Cys Gln Ser Met His Ser
500 505 510

Gln Ile Leu Gly Gly Thr Met Ile Leu Val Ile Gly Gly Ile Ile Val
515 520 525

Ala Thr Leu Leu Val Phe Ile Val Ile Leu Met Val Arg Tyr Lys Val
530 535 540

Cys Asn His Glu Ala Pro Ser Lys Met Ala Ala Ala Val Ser Asn Val
545 550 555 560

Tyr Ser Gln Thr Asn Gly Ala Gln Pro Pro Pro Pro Ser Ser Ala Pro
565 570 575

Ala Gly Ala Pro Pro
580

<210> 22
<211> 788
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown Organism: KIAA_predicted

<400> 22

Met Glu Thr Leu Leu Gly Gly Leu Leu Ala Phe Gly Met Ala Phe Ala
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Val Val Asp Ala Cys Pro Lys Tyr Cys Val Cys Gln Asn Leu Ser Glu
20 25 30

Ser Leu Gly Thr Leu Cys Pro Ser Lys Gly Leu Leu Phe Val Pro Pro
35 40 45

Asp Ile Asp Arg Arg Thr Val Glu Leu Arg Leu Gly Gly Asn Phe Ile
50 55 60

Ile His Ile Ser Arg Gln Asp Phe Ala Asn Met Thr Gly Leu Val Asp
65 70 75 80

Leu Thr Leu Ser Arg Asn Thr Ile Ser His Ile Gln Pro Phe Ser Phe
85 90 95

Leu Asp Leu Glu Ser Leu Arg Ser Leu His Leu Asp Ser Asn Arg Leu
100 105 110

Pro Ser Leu Gly Glu Asp Thr Leu Arg Gly Leu Val Asn Leu Gln His
115 120 125

Leu Ile Val Asn Asn Gln Leu Gly Gly Ile Ala Asp Glu Ala Phe
130 135 140

Glu Asp Phe Leu Leu Thr Leu Glu Asp Leu Asp Leu Ser Tyr Asn Asn
145 150 155 160

Leu His Gly Leu Pro Trp Asp Ser Val Arg Arg Met Val Asn Leu His
165 170 175

Gln Leu Ser Leu Asp His Asn Leu Leu Asp His Ile Ala Glu Gly Thr
180 185 190

Phe Ala Asp Leu Gln Lys Leu Ala Arg Leu Asp Leu Thr Ser Asn Arg
195 200 205

Leu Gln Lys Leu Pro Pro Asp Pro Ile Phe Ala Arg Ser Gln Ala Ser
210 215 220

Ala Leu Thr Ala Thr Pro Phe Ala Pro Pro Leu Ser Phe Ser Phe Gly

225 230 235 240
Gly Asn Pro Leu His Cys Asn Cys Glu Leu Leu Trp Leu Arg Arg Leu
245 250 255

Glu Arg Asp Asp Asp Leu Glu Thr Cys Gly Ser Pro Gly Gly Leu Lys
260 265 270

Gly Arg Tyr Phe Trp His Val Arg Glu Glu Glu Phe Val Cys Glu Pro
275 280 285

Pro Leu Ile Thr Gln His Thr His Lys Leu Leu Val Leu Glu Gly Gln
290 295 300

Ala Ala Thr Leu Lys Cys Lys Ala Ile Gly Asp Pro Ser Pro Leu Ile
305 310 315 320

His Trp Val Ala Pro Asp Asp Arg Leu Val Gly Asn Ser Ser Arg Thr
325 330 335

Ala Val Tyr Asp Asn Gly Thr Leu Asp Ile Phe Ile Thr Thr Ser Gln
340 345 350

Asp Ser Gly Ala Phe Thr Cys Ile Ala Ala Asn Ala Ala Gly Glu Ala
355 360 365

Thr Ala Met Val Glu Val Ser Ile Val Gln Leu Pro His Leu Ser Asn
370 375 380

Ser Thr Ser Arg Thr Ala Pro Pro Lys Ser Arg Leu Ser Asp Ile Thr
385 390 395 400

Gly Ser Ser Lys Thr Ser Arg Gly Gly Gly Ser Gly Gly Gly Glu
405 410 415

Pro Pro Lys Ser Pro Pro Glu Arg Ala Val Leu Val Ser Glu Val Thr
420 425 430

Thr Thr Ser Ala Leu Val Lys Trp Ser Val Ser Lys Ser Ala Pro Arg
435 440 445

Val Lys Met Tyr Gln Leu Gln Tyr Asn Cys Ser Asp Asp Glu Val Leu
450 455 460

Ile Tyr Arg Met Ile Pro Ala Ser Asn Lys Ala Phe Val Val Asn Asn
465 470 475 480

Leu Val Ser Gly Thr Gly Tyr Asp Leu Cys Val Leu Ala Met Trp Asp

485

490

495

Asp Thr Ala Thr Thr Leu Thr Ala Thr Asn Ile Val Gly Cys Ala Gln
500 505 510

Phe Phe Thr Lys Ala Asp Tyr Pro Gln Cys Gln Ser Met His Ser Gln
515 520 525

Ile Leu Gly Gly Thr Met Ile Leu Val Ile Gly Gly Ile Ile Val Ala
530 535 540

Thr Leu Leu Val Phe Ile Val Ile Leu Met Val Arg Tyr Lys Val Cys
545 550 555 560

Asn His Glu Ala Pro Ser Lys Met Ala Ala Ala Val Ser Asn Val Tyr
565 570 575

Ser Gln Thr Asn Gly Ala Gln Pro Pro Pro Pro Ser Ser Ala Pro Ala
580 585 590

Gly Ala Pro Pro Gln Gly Pro Pro Lys Val Val Val Arg Asn Glu Leu
595 600 605

Leu Asp Phe Thr Ala Ser Leu Ala Arg Ala Ser Asp Ser Ser Ser Ser
610 615 620

Ser Ser Leu Gly Ser Gly Glu Ala Ala Gly Leu Gly Arg Ala Pro Trp
625 630 635 640

Arg Ile Pro Pro Ser Ala Pro Arg Pro Lys Pro Ser Leu Asp Arg Leu
645 650 655

Met Gly Ala Phe Ala Ser Leu Asp Leu Lys Ser Gln Arg Lys Glu Glu
660 665 670

Leu Leu Asp Ser Arg Thr Pro Ala Gly Arg Gly Ala Gly Thr Ser Ala
675 680 685

Arg Gly His His Ser Asp Arg Glu Pro Leu Leu Gly Pro Pro Ala Ala
690 695 700

Arg Ala Arg Ser Leu Leu Pro Leu Pro Leu Glu Gly Lys Ala Lys Arg
705 710 715 720

Ser His Ser Phe Asp Met Gly Asp Phe Ala Ala Ala Gly Gly Val
725 730 735

Val Pro Gly Gly Tyr Ser Pro Pro Arg Lys Val Ser Asn Ile Trp Thr

740

745

750

Lys Arg Ser Leu Ser Val Asn Gly Met Leu Leu Pro Phe Glu Glu Ser
755 760 765

Asp Leu Val Gly Ala Arg Gly Thr Phe Gly Ser Ser Glu Trp Val Met
770 775 780

Glu Ser Thr Val
785